SEQUENCE LISTING

(1) GENERAL INFORMATION:

    (i) APPLICANT: Genentech, Inc.
                    Garrard, Lisa J.
                    Henner, Dennis J.
                    Bass, Steven
                    Greene, Ronald
                    Lowman, Henry B.
                    Wells, James A.
                    Matthews, David J.

   (ii) TITLE OF INVENTION: Enrichment Method For Variant Proteins With
          Altered Binding Properties

  (iii) NUMBER OF SEQUENCES: 27

   (iv) CORRESPONDENCE ADDRESS:
      (A) ADDRESSEE: Genentech, Inc.
      (B) STREET: 460 Point San Bruno Blvd
      (C) CITY: South San Francisco
      (D) STATE: California
      (E) COUNTRY: USA
      (F) ZIP: 94080

    (v) COMPUTER READABLE FORM:
      (A) MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
      (B) COMPUTER: IBM PC compatible
      (C) OPERATING SYSTEM: PC-DOS/MS-DOS
      (D) SOFTWARE: patin (Genentech)

   (vi) CURRENT APPLICATION DATA:
      (A) APPLICATION NUMBER:
      (B) FILING DATE: 03-DEC-91
      (C) CLASSIFICATION:

  (vii) PRIOR APPLICATION DATA:
      (A) APPLICATION NUMBER: 07/743614
      (B) APPLICATION DATE: 09-Aug-91

  (vii) PRIOR APPLICATION DATA:
      (A) APPLICATION NUMBER: 07/715300
      (B) APPLICATION DATE: 14-June-91

  (vii) PRIOR APPLICATION DATA:
      (A) APPLICATION NUMBER: 07/683400
      (B) APPLICATION DATE: 10-Apr-91

  (vii) PRIOR APPLICATION DATA:
      (A) APPLICATION NUMBER: 07/621667
      (B) APPLICATION DATE: 03-Dec-1990

 (viii) ATTORNEY/AGENT INFORMATION:
      (A) NAME: Benson, Robert H.
      (B) REGISTRATION NUMBER: 30,446
      (C) REFERENCE/DOCKET NUMBER: 645P4

   (ix) TELECOMMUNICATION INFORMATION:
      (A) TELEPHONE: 415/266-1489
      (B) TELEFAX: 415/952-9881
      (C) TELEX: 910/371-7168

(2) INFORMATION FOR SEQ ID NO:1:

    (i) SEQUENCE CHARACTERISTICS:
      (A) LENGTH: 36 bases
      (B) TYPE: nucleic acid

            (C) STRANDEDNESS: single
            (D) TOPOLOGY: linear

      (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

            GGCAGCTGTG GCTTCTAGAG TGGCGGCGGC TCTGGT 36

    (2) INFORMATION FOR SEQ ID NO:2:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 36 bases
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: single
            (D) TOPOLOGY: linear

      (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

            AGCTGTGGCT TCGGGCCCTT AGCATTTAAT GCGGTA 36

    (2) INFORMATION FOR SEQ ID NO:3:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 33 bases
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: single
            (D) TOPOLOGY: linear

      (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

            TTCACAAACG AAGGGCCCCT AATTAAAGCC AGA 33

    (2) INFORMATION FOR SEQ ID NO:4:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 30 bases
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: single
            (D) TOPOLOGY: linear

      (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

            CAATAATAAC GGGCTAGCCA AAAGAACTGG 30

    (2) INFORMATION FOR SEQ ID NO:5:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 24 bases
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: single
            (D) TOPOLOGY: linear

      (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

            CACGACAGAA TTCCCGACTG GAAA 24

    (2) INFORMATION FOR SEQ ID NO:6:

        (i) SEQUENCE CHARACTERISTICS:

          (A) LENGTH: 23 bases
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: single
          (D) TOPOLOGY: linear

5   (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

      CTGTTTCTAG AGTGAAATTG TTA 23

10

      (2) INFORMATION FOR SEQ ID NO:7:

          (i) SEQUENCE CHARACTERISTICS:
15   (A) LENGTH: 21 bases
              (B) TYPE: nucleic acid
              (C) STRANDEDNESS: single
              (D) TOPOLOGY: linear

20   (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

          ACATTCCTGG GTACCGTGCA G 21

25   (2) INFORMATION FOR SEQ ID NO:8:

          (i) SEQUENCE CHARACTERISTICS:
              (A) LENGTH: 63 bases
              (B) TYPE: nucleic acid
30   (C) STRANDEDNESS: single
              (D) TOPOLOGY: linear

       (xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

35   GCTTCAGGAA GGACATGGAC NNSGTCNNSA CANNSCTGNN SATCGTGCAG 50

40   TGCCGCTCTG TGG 63

      (2) INFORMATION FOR SEQ ID NO:9:

45   (i) SEQUENCE CHARACTERISTICS:
              (A) LENGTH: 24 bases
              (B) TYPE: nucleic acid
              (C) STRANDEDNESS: single
              (D) TOPOLOGY: linear

50   (xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

          AAGGTCTCCA CATACCTGAG GATC 24

55
      (2) INFORMATION FOR SEQ ID NO:10:

          (i) SEQUENCE CHARACTERISTICS:
60   (A) LENGTH: 33 bases
              (B) TYPE: nucleic acid
              (C) STRANDEDNESS: single
              (D) TOPOLOGY: linear

65   (xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

          ATGGACAAGG TGTCGACATA CCTGCGCATC GTG 33

(2) INFORMATION FOR SEQ ID NO:11:

    (i) SEQUENCE CHARACTERISTICS:
      (A) LENGTH: 36 bases
      (B) TYPE: nucleic acid
      (C) STRANDEDNESS: single
      (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

      GGCAGCTGTG GCTTCTAGAG TGGCGGCGGC TCTGGT 36

(2) INFORMATION FOR SEQ ID NO:12:

    (i) SEQUENCE CHARACTERISTICS:
      (A) LENGTH: 36 bases
      (B) TYPE: nucleic acid
      (C) STRANDEDNESS: single
      (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

      GGCAGCTGTG GATTCTAGAG TGGCGGTGGC TCTGGT 36

(2) INFORMATION FOR SEQ ID NO:13:

    (i) SEQUENCE CHARACTERISTICS:
      (A) LENGTH: 12 amino acids
      (B) TYPE: amino acid
      (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

Gly Ser Cys Gly Phe Glu Ser Gly Gly Gly Ser Gly
1   5   10   12

(2) INFORMATION FOR SEQ ID NO:14:

    (i) SEQUENCE CHARACTERISTICS:
      (A) LENGTH: 27 bases
      (B) TYPE: nucleic acid
      (C) STRANDEDNESS: single
      (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

      CGGACTGGGC AGATATTCAA GCAGACC 27

(2) INFORMATION FOR SEQ ID NO:15:

    (i) SEQUENCE CHARACTERISTICS:
      (A) LENGTH: 38 bases
      (B) TYPE: nucleic acid
      (C) STRANDEDNESS: single
      (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

      CTCAAGAACT ACGGGTTACC CTGACTGCTT CAGGAAGG 38

(2) INFORMATION FOR SEQ ID NO:16:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 30 bases
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

        CGCATCGTGC AGTGCAGATC TGTGGAGGGC 30

(2) INFORMATION FOR SEQ ID NO:17:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 66 bases
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

        GTTACTCTAC TGCTTTCAGG AAGGACATGG ACNNSGTCNN SACANNSCTG 50

        NNSATCGTGC AGTGCA 66

(2) INFORMATION FOR SEQ ID NO:18:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 64 bases
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

        GATCTGCACT GCACGATSNN CAGSNNTGTS NNGACSNNGT CCATGTCCTT 50

        CCTGAAGCAG TAGA 64

(2) INFORMATION FOR SEQ ID NO:19:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 25 bases
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

        GCCTTTGACA GGTACCAGGA GTTTG 25

(2) INFORMATION FOR SEQ ID NO:20:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 33 bases

        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

        CCAACTATAC CACTCTCGAG GTCTATTCGA TAA 33

(2) INFORMATION FOR SEQ ID NO:21:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 66 bases
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

        TCGAGGCTCN NSGACAACGC GNNSCTGCGT GCTNNSCGTC TTNNSCAGCT 50

        GGCCTTTGAC ACGTAC 66

(2) INFORMATION FOR SEQ ID NO:22:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 58 bases
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

        GTGTCAAAGG CCAGCTGSNN AAGACGSNNA GCACGCAGSN NCGCGTTGTC 50

        SNNGAGCC 58

(2) INFORMATION FOR SEQ ID NO:23:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 65 bases
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

        GTTACTCTAC TGCTTCNNSA AGGACATGNN SAAGGTCAGC NNSTACCTGC 50

        GCNNSGTGCA GTGCA 65

(2) INFORMATION FOR SEQ ID NO:24:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 64 bases
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

GATCTGCACT GCACSNNGCG CAGGTASNNG CTGACCTTSN NCATGTCCTT 50

SNNGAAGCAG TAGA 64

(2) INFORMATION FOR SEQ ID NO:25:

    (i) SEQUENCE CHARACTERISTICS:
       (A) LENGTH: 2178 bases
       (B) TYPE: nucleic acid
       (C) STRANDEDNESS: single
       (D) TOPOLOGY: linear

   (xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

ATGAAAAAGA ATATCGCATT TCTTCTTGCA TCTATGTTCG TTTTTTCTAT 50

TGCTACAAAC GCGTACGCTG ATATCCAGAT GACCCAGTCC CCGAGCTCCC 100

TGTCCGCCTC TGTGGGCGAT AGGGTCACCA TCACCTGCCG TGCCAGTCAG 150

GATGTGAATA CTGCTGTAGC CTGGTATCAA CAGAAACCAG GAAAAGCTCC 200

GAAACTACTG ATTTACTCGG CATCCTTCCT CTACTCTGGA GTCCCTTCTC 250

GCTTCTCTGG ATCCAGATCT GGGACGGATT TCACTCTGAC CATCAGCAGT 300

CTGCAGCCGG AAGACTTCGC AACTTATTAC TGTCAGCAAC ATTATACTAC 350

TCCTCCCACG TTCGGACAGG GTACCAAGGT GGAGATCAAA CGAACTGTGG 400

CTGCACCATC TGTCTTCATC TTCCCGCCAT CTGATGAGCA GTTGAAATCT 450

GGAACTGCCT CTGTTGTGTG CCTGCTGAAT AACTTCTATC CCAGAGAGGC 500

CAAAGTACAG TGGAAGGTGG ATAACGCCCT CCAATCGGGT AACTCCCAGG 550

AGAGTGTCAC AGAGCAGGAC AGCAAGGACA GCACCTACAG CCTCAGCAGC 600

ACCCTGACGC TGAGCAAAGC AGACTACGAG AAACACAAAG TCTACGCCTG 650

CGAAGTCACC CATCAGGGCC TGAGCTCGCC CGTCACAAAG AGCTTCAACA 700

GGGGAGAGTG TTAAGCTGAT CCTCTACGCC GGACGCATCG TGGCCCTAGT 750

ACGCAAGTTC ACGTAAAAAG GGTATCTAGA GGTTGAGGTG ATTTATGAA 800

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AAAGAATATC GCATTTCTTC TTGCATCTAT GTTCGTTTTT TCTATTGCTA 850

CAAACGCGTA CGCTGAGGTT CAGCTGGTGG AGTCTGGCGG TGGCCTGGTG 900

CAGCCAGGGG GCTCACTCCG TTTGTCCTGT GCAGCTTCTG GCTTCAACAT 950

TAAAGACACC TATATACACT GGGTGCGTCA GGCCCCGGGT AAGGGCCTGG 1000

AATGGGTTGC AAGGATTTAT CCTACGAATG GTTATACTAG ATATGCCGAT 1050

AGCGTCAAGG GCCGTTTCAC TATAAGCGCA GACACATCCA AAAACACAGC 1100

CTACCTGCAG ATGAACAGCC TGCGTGCTGA GGACACTGCC GTCTATTATT 1150

GTTCTAGATG GGGAGGGGAC GGCTTCTATG CTATGGACTA CTGGGGTCAA 1200

GGAACCCTGG TCACCGTCTC CTCGGCCTCC ACCAAGGGCC CATCGGTCTT 1250

CCCCCTGGCA CCCTCCTCCA AGAGCACCTC TGGGGGCACA GCGGCCCTGG 1300

GCTGCCTGGT CAAGGACTAC TTCCCCGAAC CGGTGACGGT GTCGTGGAAC 1350

TCAGGCGCCC TGACCAGCGG CGTGCACACC TTCCCGGCTG TCCTACAGTC 1400

CTCAGGACTC TACTCCCTCA GCAGCGTGGT GACTGTGCCC TCTAGCAGCT 1450

TGGGCACCCA GACCTACATC TGCAACGTGA ATCACAAGCC CAGCAACACC 1500

AAGGTGGACA AGAAAGTTGA GCCCAAATCT TGTGACAAAA CTCACACAGG 1550

GCCCTTCGTT TGTGAATATC AAGGCCAATC GTCTGACCTG CCTCAACCTC 1600

CTGTCAATGC TGGCGGCGGC TCTGGTGGTG GTTCTGGTGG CGGCTCTGAG 1650

GGTGGTGGCT CTGAGGGTGG CGGTTCTGAG GGTGGCGGCT CTGAGGGAGG 1700

CGGTTCCGGT GGTGGCTCTG GTTCCGGTGA TTTTGATTAT GAAAAGATGG 1750

CAAACGCTAA TAAGGGGGCT ATGACCGAAA ATGCCGATGA AAACGCGCTA 1800

CAGTCTGACG CTAAAGGCAA ACTTGATTCT GTCGCTACTG ATTACGGTGC 1850

TGCTATCGAT GGTTTCATTG GTGACGTTTC CGGCCTTGCT AATGGTAATG 1900

GTGCTACTGG TGATTTTGCT GGCTCTAATT CCCAAATGGC TCAAGTCGGT 1950
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GACGGTGATA ATTCACCTTT AATGAATAAT TTCCGTCAAT ATTTACCTTC 2000

CCTCCCTCAA TCGGTTGAAT GTCGCCCTTT TGTCTTTAGC GCTGGTAAAC 2050

CATATGAATT TTCTATTGAT TGTGACAAAA TAAACTTATT CCGTGGTGTC 2100

TTTGCGTTTC TTTTATATGT TGCCACCTTT ATGTATGTAT TTTCTACGTT 2150

TGCTAACATA CTGCGTAATA AGGAGTCT 2178

(2) INFORMATION FOR SEQ ID NO:26:

   (i) SEQUENCE CHARACTERISTICS:
     (A) LENGTH: 237 amino acids
     (B) TYPE: amino acid
     (D) TOPOLOGY: linear

   (xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

Met Lys Lys Asn Ile Ala Phe Leu Leu Ala Ser Met Phe Val Phe
1   5   10   15

Ser Ile Ala Thr Asn Ala Tyr Ala Asp Ile Gln Met Thr Gln Ser
            20   25   30

Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr
                35   40   45

Cys Arg Ala Ser Gln Asp Val Asn Thr Ala Val Ala Trp Tyr Gln
            50   55   60

Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Ser Ala Ser
                65   70   75

Phe Leu Tyr Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Arg Ser
                80   85   90

Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp
            95   100   105

Phe Ala Thr Tyr Tyr Cys Gln Gln His Tyr Thr Thr Pro Pro Thr
            110   115   120

Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala
            125   130   135

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser
            140   145   150

Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg
            155   160   165

Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly
            170   175   180

Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr
            185   190   195

Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu
            200   205   210

Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser
            215   220   225

Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
             230   235   237

(2) INFORMATION FOR SEQ ID NO:27:

   (i) SEQUENCE CHARACTERISTICS:
       (A) LENGTH: 461 amino acids
       (B) TYPE: amino acid
       (D) TOPOLOGY: linear

   (xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

Met Lys Lys Asn Ile Ala Phe Leu Leu Ala Ser Met Phe Val Phe
  1   5   10   15

Ser Ile Ala Thr Asn Ala Tyr Ala Glu Val Gln Leu Val Glu Ser
             20   25   30

Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys
             35   40   45

Ala Ala Ser Gly Phe Asn Ile Lys Asp Thr Tyr Ile His Trp Val
             50   55   60

Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Tyr
             65   70   75

Pro Thr Asn Gly Tyr Thr Arg Tyr Ala Asp Ser Val Lys Gly Arg
             80   85   90

Phe Thr Ile Ser Ala Asp Thr Ser Lys Asn Thr Ala Tyr Leu Gln
             95   100   105

Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ser
             110   115   120

Arg Trp Gly Gly Asp Gly Phe Tyr Ala Met Asp Tyr Trp Gly Gln
             125   130   135

Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser
             140   145   150

Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr
             155   160   165

Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val
             170   175   180

Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr
             185   190   195

Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser
             200   205   210

Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile
             215   220   225

Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys
             230   235   240

Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Gly Pro Phe Val
             245   250   255

Cys Glu Tyr Gln Gly Gln Ser Ser Asp Leu Pro Gln Pro Pro Val
             260   265   270

Asn Ala Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Glu
             275   280   285

Gly Gly Gly Ser Glu Gly Gly Gly Ser Glu Gly Gly Gly Ser Glu
                290   295   300

Gly Gly Gly Ser Gly Gly Gly Ser Gly Ser Gly Asp Phe Asp Tyr
                305   310   315

Glu Lys Met Ala Asn Ala Asn Lys Gly Ala Met Thr Glu Asn Ala
                320   325   330

Asp Glu Asn Ala Leu Gln Ser Asp Ala Lys Gly Lys Leu Asp Ser
                335   340   345

Val Ala Thr Asp Tyr Gly Ala Ala Ile Asp Gly Phe Ile Gly Asp
                350   355   360

Val Ser Gly Leu Ala Asn Gly Asn Gly Ala Thr Gly Asp Phe Ala
                365   370   375

Gly Ser Asn Ser Gln Met Ala Gln Val Gly Asp Gly Asp Asn Ser
                380   385   390

Pro Leu Met Asn Asn Phe Arg Gln Tyr Leu Pro Ser Leu Pro Gln
                395   400   405

Ser Val Glu Cys Arg Pro Phe Val Phe Ser Ala Gly Lys Pro Tyr
                410   415   420

Glu Phe Ser Ile Asp Cys Asp Lys Ile Asn Leu Phe Arg Gly Val
                425   430   435

Phe Ala Phe Leu Leu Tyr Val Ala Thr Phe Met Tyr Val Phe Ser
                440   445   450

Thr Phe Ala Asn Ile Leu Arg Asn Lys Glu Ser
                455   460 461